

RAW SEQUENCE LISTING

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Application Serial Number: 10/073,064
Source: /FW/6
Date Processed by STIC: 9/28/05

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PAGE: 1

**RAW SEQUENCE LISTING
PATENT APPLICATION US/10/073,064**

DATE: 09/28/2005
TIME: 15:59:28

INPUT SET: S30741.raw

This Raw Listing contains the General Information Section and up to the first 5 pages.

SEQUENCE LISTING

1
2
3 (1) General Information:
4 (i) APPLICANT: Ciossek, Thomas
5 Ullrich, Axel
6 Millauer, Birgit
7 (ii) TITLE OF INVENTION: METHODS FOR DIAGNOSIS
8 AND TREATMENT OF MDK
9 SIGNAL TRANSDUCTION
10 DISORDERS
11 (iii) NUMBER OF SEQUENCES: 12
12 (iv) CORRESPONDENCE ADDRESS:
13 (A) ADDRESSEE: Lyon & Lyon
14 (B) STREET: 633 West Fifth Street
15 Suite 4700
16 (C) CITY: Los Angeles
17 (D) STATE: California
18 (E) COUNTRY: U.S.A.
19 (F) ZIP: 90071-2066
20 (v) COMPUTER READABLE FORM:
21 (A) MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
22 storage
23 (B) COMPUTER: IBM Compatible
24 (C) OPERATING SYSTEM: IBM P.C. DOS 5.0
25 (D) SOFTWARE: Word Perfect 5.1
26 (vi) CURRENT APPLICATION DATA:
27 (A) APPLICATION NUMBER: US/10/073,064
28 (B) FILING DATE: 12-Feb-2002
29 (C) CLASSIFICATION: 435
30 (vii) PRIOR APPLICATION DATA:
31 (A) APPLICATION NUMBER: US/08/438,265
32 (B) FILING DATE: MAY 9, 1995
33 (A) APPLICATION NUMBER: US/08/368,776
34 (B) FILING DATE: January 3, 1995
35 (A) APPLICATION NUMBER: <Unknown>
36 (B) FILING DATE: <Unknown>
37 (viii) ATTORNEY/AGENT INFORMATION:
38 (A) NAME: Warburg, Richard J.
39 (B) REGISTRATION NUMBER: 32,327
40 (C) REFERENCE/DOCKET NUMBER: 208/007
41 (ix) TELECOMMUNICATION INFORMATION:
42 (A) TELEPHONE: (213) 489-1600
43 (B) TELEFAX: (213) 955-0440
44 (C) TELEX: 67-3510
45 (2) INFORMATION FOR SEQ ID NO: 1:
46 (i) SEQUENCE CHARACTERISTICS:

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47	(A) LENGTH: 4304 base pairs	
48	(B) TYPE: nucleic acid	
49	(C) STRANDEDNESS: single	
50	(D) TOPOLOGY: linear	
51	(ii) MOLECULE TYPE: nucleic	
52	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:	
53	AAGCGGCCGG TCTGCAGTCG GAGACTGCA GGCAGCAAC ACGGTGCGAA	50
54	CGAACCGGAG GGGGGAGAGA GAAATCAAAC AGCTAACGCGT GGAGCAGACG	100
55	GCCTGGGACC CAGAAGGGGA TCGATGCGAG GAGCGCAATA ATAACAACAA	150
56	TAATAACCCA CTTCGGAGCA AACAGCATCT AAAGAGCTGC GACCCAACGT	200
57	CAGCCTAAAA AAATCAAAC TGCTCATGCA CCATGGTTGT TCAAACCTGG	250
58	TTCCCTTCGT GGATTATTTC GTGTTACATC TGGCTGCTTG GCTTGCACA	300
59	CACGGGGAG GCGCAGGCTG CGAAGGAAGT ACTATTACTG GACTCGAAAG	350
60	CACAACAAAC AGAATTGGAA TGGATTCCT CTCCACCCAG TGGGTGGAA	400
61	GAAATTAGTG GTTGGATGA GAACTACACT CCGATAAGAA CATAACCAGGT	450
62	GTGCCAGGTC ATGGAGCCC ACCAGAACAA CTGGCTGCGG ACTAACTGGA	500
63	TTTCTAAAGG CAACGCACAA AGGATTTTG TAGAATTGAA ATTACACCTT	550
64	AGGGATTGTA ATAGTCTTCC CGGAGTCCTG GGAACTTGCA AGGAAACGTT	600
65	TAATTGTAC TATTATGAAA CAGACTACGA CACCGGCAGG AATATACGAG	650
66	AAAACCTTTA TGTTAAAATA GACACCATTG CTGCAGATGA AAGTTTCACA	700
67	CAAGGTGACC TTGGTGAAG AAAGATGAAG CTGAACACTG AGGTGAGAGA	750
68	GATTGGACCT TTGTCAAAA AGGGATTCTA TCTTGCCTT CAGGATGTAG	800
69	GGGCTTCAT AGCATTGGTT TCTGTCAAAG TGTACTACAA GAAGTGTGCG	850
70	ACCATTGTTG AGAACATTAGC TGTCTTCCA GATACAGTGA CTGGTTCGGA	900
71	ATTTTCTCC TTAGTCGAGG TCCGTGGAC ATGTGTCAAG AGTGCCGAGG	950
72	AAGAGGCAGA AAATTCCCCC AGAATGCATT GCAGTGCAGA AGGAGAGTGG	1000
73	CTAGTACCCA TTGGAAAATG CATCTGCAAA GCAGGCTATC AGCAAAAAGG	1050
74	GGACACTTGC GAACCCCTGTG GCCGCAGGTT CTACAAATCT TCCTCTCAGG	1100
75	ATCTCCAGTG TTCTCGTTGT CCAACCCACA GCTTCTCTGA CCGAGAAGGA	1150
76	TCATCCAGGT GTGAATGTGA AGATGGGTAC TACAGAGCTC CTTCTGATCC	1200
77	ACCATACGTT GCATGCACGA GGCCTCCCTC TGCAACCACAG AACCTTATT	1250
78	TCAATATCAA TCAAAACGACT GTAAGTTGG AATGGAGTCC TCCGGCTGAC	1300
79	AACGGGGAA GAAACGATGT CACCTACAGA ATACTGTGA AGCGGTGCAG	1350
80	TTGGGAACAG GGAGAATGTG TGCCATGCGG AAGTAACATT GGATACATGC	1400
81	CCCAGCAGAC GGGATTAGAG GATAACTATG TCACTGTAT GGACCTACTT	1450
82	GCCCATGCAA ATTACACTTT CGAAGTTGAA GCTGTAAATG GAGTTTCAGG	1500
83	CTTAAGCAGA TCCCAGAGGC TCTTCGCTGC TGTTAGCATC ACCACCGGT	1550
84	AAGCAGCTCC CTCGCAAGTG AGTGGAGTCA TGAAGGAGCG AGTACTGCAG	1600
85	CGGAGTGTGC AGCTTCTCG GCAGGAGCCG GAGCATCCA ATGGAGTCAT	1650
86	CACGGAATAT GAAATCAAGT ATTATGAGAA AGATCAACGG GAAAGGACGT	1700
87	ACTCAACACT CAAAACCAAG TCCACCTCCG CCTCCATCAA TAATCTGAAA	1750
88	CCGGGAACAG TGTACGTCTT TCAGATCCGG GCGGTCACTG CTGGCGGTTA	1800
89	TGAAACTAC AGCCCTAGGC TTGATGTTGC CACACTTGAG GAAGCTTCAG	1850
90	GTAAAATGTT TGAAGCGACA GCAGTCTCCA GTGAACAGAA TCCGTATC	1900
91	ATAATTGCTG TAGTGGCTGT AGCAGGGACC ATCATCTTGG TGTTCATGGT	1950
92	GTTCGGCTTC ATCATTGGAA GAAGGCACTG TGGTTATAGC AAGGCTGACC	2000
93	AAGAAGGGGA TGAAGAACTC TACTTTCTT TTAAATTTC AGGCACCAAA	2050
94	ACCTACATTG ACCCTGAAAC CTATGAGGAC CCAAATAGAG CTGTCCATCA	2100
95	ATTGCCAAG GAGCTAGATG CCTCTGTAT TAAAATTGAG CGTGTGATTG	2150
96	GTGCAGGAGA ATTTGGAGAA GTTGCAGTG GTCGTTGAA ACTTCCGGGC	2200
97	CAGAGAGATG TTGCAGTGGC CATAAAAACC CTGAAAGTTG GTTACACAGA	2250
98	AAAGCAAAGG AGGGACTTTT TATGCGAACG AAGCATCATG GGGCAATTG	2300
99	ACCACCCAAA TGTCGTCCAT TTGGAAGGGG TTGTTACAAG AGGGAAGCCT	2350

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100	GTCATGATTG TGATAGAGTT CATGGAGAAT GGAGCCCTGG ATGCATTTCT	2400
101	CAGGAAACAC GATGGGCAGT TTACAGTCAT TCAGTTGGA GGAATGTTGA	2450
102	GAGGTATTGC CGCTGGGATG CGATACTTGG CTGATATGGG ATACGTTCAC	2500
103	AGGGACCTTG CAGCGCGCAA CATCCTTGTCA AACAGCAATC TTGTTTGTAA	2550
104	AGTGTCAAGAT TTTGGCCTT CCCGGTTAT AGAGGATGAT CCCGAAGCTG	2600
105	TCTACACCAC GACTGGTCCA AAAATTCCAG TAAGGTGGAC TGCAACCGGAA	2650
106	GCCATTCAAT ACCCGGAAGTT CACCTCAGCC AGCGATGTGT GGAGCTATGG	2700
107	GATTGTCAATG TGGGAAGTGA TGTCTTATGG AGAAAGACCT TACTGGGACA	2750
108	TGTCAAATCA AGATGTCAATT AAAGCGATAG AAGAAGGTTA TCGTTGCCG	2800
109	GCGCCCATGG ATTGCCCAAGC TGGTCTTCAC CAGCTAATGC TGGATTGTTG	2850
110	GCAGAAAAGAT CGGGCGGAAA GGCCAAAGTT TGAGCAGATA GTCGGAATTC	2900
111	TAGACAAAAT GATTGAAAC CCAAGTAGTC TGAAAACACC CCTGGGAACT	2950
112	TGTAGTAGAC CCTTAAGCCC TCTTCTGGAC CAGAGCACTC CTGACTTCAC	3000
113	TGCCTCTGT TCAGTTGGAG AATGGTTGCA AGCTATTAAGG ATGAAAGGTT	3050
114	ATAAGGACAA CTTCACAGCA GCGGGTTACA ACTCACTCGA GTCAGTGGCC	3100
115	AGGATGACTA TCGATGATGT GATGAGTTA GGGATCACAC TGGTTGGCCA	3150
116	TCAAAAGAAG ATCATGAGCA GCATCCAGAC TATGCGGGCA CAAATGTTGC	3200
117	ATTTACACGG AACAGGCATC CAAGTGTGAC ACATCGGCCT CCCTCAGATG	3250
118	AGGCTTAAGA CTGCAGGAGA ACAGTTCTGG CCTTCAGTAT ACGCATAGAA	3300
119	TGCTGCTAGA AGACAGTTGA TATACTGGGT CCTTCCTACA AGAAAGAGAA	3350
120	GATTTAGAA GCACCTCCAG ACTTGAACCTC CTAAGTGCCA CCAGAATATA	3400
121	CAAAAAGGGA ATTTAGGATC CACCACTGGT GGCCAGGAAC ACAGCAGAGA	3450
122	CAATAAACAA AGTACTACCT GAAAAACATC CCAACACCTT GAGCTCTCGA	3500
123	ACCTCTTTT TATCTTATAG ACTTTTTAAA AATGTACATA AAGAATTAA	3550
124	GAAAGAATAT ATTTGTCAA TAAAATCAT GATCTTATTG TTAAAATCAA	3600
125	TGAAATATTT TCCTTAAAAT ATGTGATTTC AGACTATTCT TTTCAGAAC	3650
126	CATCTGTGTT TATTCTGCTT AAGGACTTTG TTTTAGAAAG TTATTGTAG	3700
127	CTTTGGACCT TTTTAGTGTAA AATTTATGA CACGTTACTA CACTGGGAAC	3750
128	CTTTGAAGAC TCTCAAACCTT AAAGGAAAGC AAAACTACGC ACATAGTCGA	3800
129	GGATGGACTT TGTCTTCAT GGCTTGGTA TCCTGGCTGT GTCATTTGT	3850
130	TAAACCAAGTG ATGTTTCAT ATTGTTTGCT GATTGGCAGG TAGTTCAAAA	3900
131	TTGCAAGTTG CCAAGAGCTC TGATATTTTT TAACAGGATT TTTTTCTT	3950
132	TGTAAAATC AGATAAACATA CTAACTTTTC AATGAAAAAA AAAAAAAAG	4000
133	AAGCAATAAT GATCCATAAA TACTATAAGG CACTTTAAC AGATTGTTA	4050
134	TAGAGTGATT TACTAGGCAG AATTAAATAA AAAAAAAAGA GAGATGTCAA	4100
135	ATTTTAGGTT TATGTGTATA TGATAAAAGG CTGAGCTTCG TCTGAAGATG	4150
136	CTGGTGAAGAG CAAGACTGGA AGCGAAGCTC TCCAGCTTG GCTAACCCAA	4200
137	TCCGAGCACA TCAAGAGCTT CAGTCTTGTG ACAGTAAGAA ATTTAGGAAC	4250
138	ATAGTTGACC TATATTTGT ATTCTTCTT GTTGAATGCA GTCCAAATAC	4300
139	AAAA	4304
140		

141 (2) INFORMATION FOR SEQ ID NO: 2:

142 (i) SEQUENCE CHARACTERISTICS:

- 143 (A) LENGTH: 998 amino acids
- 144 (B) TYPE: amino acid
- 145 (C) STRANDEDNESS: single
- 146 (D) TOPOLOGY: linear

147 (ii) MOLECULE TYPE: peptide

148 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

149	Met Val Val Gln Thr Arg Phe Pro Ser Trp Ile Ile Leu Cys Tyr Ile			
150	1	5	10	15
151	Trp Leu Leu Gly Phe Ala His Thr Gly Glu Ala Gln Ala Ala Lys Glu			
152	20	25	30	

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153 Val Leu Leu Leu Asp Ser Lys Ala Gln Gln Thr Glu Leu Glu Trp Ile
154      35          40          45
155 Ser Ser Pro Pro Ser Gly Trp Glu Glu Ile Ser Gly Leu Asp Glu Asn
156      50          55          60
157 Tyr Thr Pro Ile Arg Thr Tyr Gln Val Cys Gln Val Met Glu Pro Asn
158      65          70          75          80
159 Gln Asn Asn Trp Leu Arg Thr Asn Trp Ile Ser Lys Gly Asn Ala Gln
160      85          90          95
161 Arg Ile Phe Val Glu Leu Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu
162      100         105         110
163 Pro Gly Val Leu Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Tyr
164      115         120         125
165 Glu Thr Asp Tyr Asp Thr Gly Arg Asn Ile Arg Glu Asn Leu Tyr Val
166      130         135         140
167 Lys Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Gly Asp Leu
168      145         150         155         160
169 Gly Glu Arg Lys Met Lys Leu Asn Thr Glu Val Arg Glu Ile Gly Pro
170      165         170         175
171 Leu Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys
172      180         185         190
173 Ile Ala Leu Val Ser Val Lys Val Tyr Tyr Lys Lys Cys Trp Thr Ile
174      195         200         205
175 Val Glu Asn Leu Ala Val Phe Pro Asp Thr Val Thr Gly Ser Glu Phe
176      210         215         220
177 Ser Ser Leu Val Glu Val Arg Gly Thr Cys Val Ser Ser Ala Glu Glu
178      225         230         235         240
179 Glu Ala Glu Asn Ser Pro Arg Met His Cys Ser Ala Glu Gly Glu Trp
180      245         250         255
181 Leu Val Pro Ile Gly Lys Cys Ile Cys Lys Ala Gly Tyr Gln Gln Lys
182      260         265         270
183 Gly Asp Thr Cys Glu Pro Cys Gly Arg Arg Phe Tyr Lys Ser Ser Ser
184      275         280         285
185 Gln Asp Leu Gln Cys Ser Arg Cys Pro Thr His Ser Phe Ser Asp Arg
186      290         295         300
187 Glu Gly Ser Ser Arg Cys Glu Cys Glu Asp Gly Tyr Tyr Arg Ala Pro
188      305         310         315         320
189 Ser Asp Pro Pro Tyr Val Ala Cys Thr Arg Pro Pro Ser Ala Pro Gln
190      325         330         335
191 Asn Leu Ile Phe Asn Ile Asn Gln Thr Thr Val Ser Leu Glu Trp Ser
192      340         345         350
193 Pro Pro Ala Asp Asn Gly Gly Arg Asn Asp Val Thr Tyr Arg Ile Leu
194      355         360         365
195 Cys Lys Arg Cys Ser Trp Glu Gln Gly Glu Cys Val Pro Cys Gly Ser
196      370         375         380
197 Asn Ile Gly Tyr Met Pro Gln Gln Thr Gly Leu Glu Asp Asn Tyr Val
198      385         390         395         400
199 Thr Val Met Asp Leu Leu Ala His Ala Asn Tyr Thr Phe Glu Val Glu
200      405         410         415
201 Ala Val Asn Gly Val Ser Asp Leu Ser Arg Ser Gln Arg Leu Phe Ala
202      420         425         430
203 Ala Val Ser Ile Thr Thr Gly Gln Ala Ala Pro Ser Gln Val Ser Gly
204      435         440         445
205 Val Met Lys Glu Arg Val Leu Gln Arg Ser Val Gln Leu Ser Trp Gln

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206	450	455	460
207	Glu Pro Glu His Pro Asn Gly Val Ile Thr Glu Tyr Glu Ile Lys Tyr		
208	465	470	475
			480
209	Tyr Glu Lys Asp Gln Arg Glu Arg Thr Tyr Ser Thr Leu Lys Thr Lys		
210	485	490	495
211	Ser Thr Ser Ala Ser Ile Asn Asn Leu Lys Pro Gly Thr Val Tyr Val		
212	500	505	510
213	Phe Gln Ile Arg Ala Val Thr Ala Ala Gly Tyr Gly Asn Tyr Ser Pro		
214	515	520	525
215	Arg Leu Asp Val Ala Thr Leu Glu Ala Ser Gly Lys Met Phe Glu		
216	530	535	540
217	Ala Thr Ala Val Ser Ser Glu Gln Asn Pro Val Ile Ile Ile Ala Val		
218	545	550	555
			560
219	Val Ala Val Ala Gly Thr Ile Ile Leu Val Phe Met Val Phe Gly Phe		
220	565	570	575
221	Ile Ile Gly Arg Arg His Cys Gly Tyr Ser Lys Ala Asp Gln Glu Gly		
222	580	585	590
223	Asp Glu Glu Leu Tyr Phe His Phe Lys Phe Pro Gly Thr Lys Thr Tyr		
224	595	600	605
225	Ile Asp Pro Glu Thr Tyr Glu Asp Pro Asn Arg Ala Val His Gln Phe		
226	610	615	620
227	Ala Lys Glu Leu Asp Ala Ser Cys Ile Lys Ile Glu Arg Val Ile Gly		
228	625	630	635
			640
229	Ala Gly Glu Phe Gly Glu Val Cys Ser Gly Arg Leu Lys Leu Pro Gly		
230	645	650	655
231	Gln Arg Asp Val Ala Val Ala Ile Lys Thr Leu Lys Val Gly Tyr Thr		
232	660	665	670
233	Glu Lys Gln Arg Arg Asp Phe Leu Cys Glu Ala Ser Ile Met Gly Gln		
234	675	680	685
235	Phe Asp His Pro Asn Val Val His Leu Glu Gly Val Val Thr Arg Gly		
236	690	695	700
237	Lys Pro Val Met Ile Val Ile Glu Phe Met Glu Asn Gly Ala Leu Asp		
238	705	710	715
			720
239	Ala Phe Leu Arg Lys His Asp Gly Gln Phe Thr Val Ile Gln Leu Val		
240	725	730	735
241	Gly Met Leu Arg Gly Ile Ala Ala Gly Met Arg Tyr Leu Ala Asp Met		
242	740	745	750
243	Gly Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Asn Ser		
244	755	760	765
245	Asn Leu Val Cys Lys Val Ser Asp Phe Gly Leu Ser Arg Val Ile Glu		
246	770	775	780
247	Asp Asp Pro Glu Ala Val Tyr Thr Thr Gly Gly Lys Ile Pro Val		
248	785	790	795
			800
249	Arg Trp Thr Ala Pro Glu Ala Ile Gln Tyr Arg Lys Phe Thr Ser Ala		
250	805	810	815
251	Ser Asp Val Trp Ser Tyr Gly Ile Val Met Trp Glu Val Met Ser Tyr		
252	820	825	830
253	Gly Glu Arg Pro Tyr Trp Asp Met Ser Asn Gln Asp Val Ile Lys Ala		
254	835	840	845
255	Ile Glu Glu Gly Tyr Arg Leu Pro Ala Pro Met Asp Cys Pro Ala Gly		
256	850	855	860
257	Leu His Gln Leu Met Leu Asp Cys Trp Gln Lys Asp Arg Ala Glu Arg		
258	865	870	875
			880